FIGURE 1A

```
  1 CGCGGGGTGT TCTGGTGTCC CCCGCCCCGC CTCTCCAAAA AGCTACACCG ACGCGGACCG
    GCGCCCCACA AGACCACAGG GGGCGGGGCG GAGAGGTTTT TCGATGTGGC TGCGCCTGGC
```

```
                                                                      sstI
 61 CGGCGGCGTC CTCCCTCGCC CTCGCTTCAC CTCGCGGGCT CCGAATGCGG GGAGCTCGGA
    GCCGCCGCAG GAGGGAGCGG GAGCGAAGTG GAGCGCCCGA GGCTTACGCC CCTCGAGCCT
```

```
121 TGTCCGGTTT CCTGTGAGGC TTTTACCTGA CACCCGCCGC CTTTCCCCGG CACTGGCTGG
    ACAGGCCAAA GGACACTCCG AAAATGGACT GTGGGCGGCG GAAAGGGGCC GTGACCGACC
```

```
    kasI
181 GAGGGCGCCC TGCAAAGTTG GGAACGCGGA GCCCCGGACC CGCTCCCGCC GCCTCCGGCT
    CTCCCGCGGG ACGTTTCAAC CCTTGCGCCT CGGGGCCTGG GCGAGGGCGG CGGAGGCCGA
```

```
241 CGCCCAGGGG GGGTCGCCGG GAGGAGCCCG GGGGAGAGGG ACCAGGAGGG GCCCGCGGCC
    GCGGGTCCCC CCCAGCGGCC CTCCTCGGGC CCCCTCTCCC TGGTCCTCCC CGGGCGCCGG
```

```
    kasI                             ageI
301 TCGCAGGGGC GCCCGCGCCC CCACCCCTGC CCCCGCCAGC GGACCGGTCC CCCACCCCCG
    AGCGTCCCCG CGGGCGCGGG GGTGGGGACG GGGGCGGTCG CCTGGCCAGG GGGTGGGGGC
```

```
361 GTCCTTCCAC CATGCACTTG CTGGGCTTCT TCTCTGTGGC GTGTTCTCTG CTCGCCGCTG
    CAGGAAGGTG GTACGTGAAC GACCCGAAGA AGAGACACCG CACAAGAGAC GAGCGGCGAC
-20          M   H   L   L   G   F   F   S   V   A   C   S   L   L   A   A   A
```

```
                          kasI
421 CGCTGCTCCC GGGTCCTCGC GAGGCGCCCG CCGCCGCCGC CGCCTTCGAG TCCGGACTCG
    GCGACGAGGG CCCAGGAGCG CTCCGCGGGC GGCGGCGGCG GCGGAAGCTC AGGCCTGAGC
 -3  L   L   P   G   P   R   E   A   P   A   A   A   A   A   F   E   S   G   L   D
```

```
481 ACCTCTCGGA CGCGGAGCCC GACGCGGGCG AGGCCACGGC TTATGCAAGC AAAGATCTGG
    TGGAGAGCCT GCGCCTCGGG CTGCGCCCGC TCCGGTGCCG AATACGTTCG TTTCTAGAGC
 18  L   S   D   A   E   P   D   A   G   E   A   T   A   Y   A   S   K   D   L   E
```

```
541 AGGAGCAGTT ACGGTCTGTG TCCAGTGTAG ATGAACTCAT GACTGTACTC TACCCAGAAT
    TCCTCGTCAA TGCCAGACAC AGGTCACATC TACTTGAGTA CTGACATGAG ATGGGTCTTA
 38  E   Q   L   R   S   V   S   S   V   D   E   L   M   T   V   L   Y   P   E   Y
```

```
601 ATTGGAAAAT GTACAAGTGT CAGCTAAGGA AAGGAGGCTG GCAACATAAC AGAGAACAGG
    TAACCTTTTA CATGTTCACA GTCGATTCCT TTCCTCCGAC CGTTGTATTG TCTCTTGTCC
 58  W  K  M   Y  K  C   Q  L  R   K  G  G   W  Q  H   N  R  E   Q  A


661 CCAACCTCAA CTCAAGGACA GAAGAGACTA TAAAATTTGC TGCAGCACAT TATAATACAG
    GGTTGGAGTT GAGTTCCTGT CTTCTCTGAT ATTTTAAACG ACGTCGTGTA ATATTATGTC
 78  N  L  N   S  R  T   E  E  T   I  K  F   A  A  A   H  T  N   T  E


                                                        sphI
721 AGATCTTGAA AAGTATTGAT AATGAGTGGA GAAAGACTCA ATGCATGCCA CGGGAGGTGT
    TCTAGAACTT TTCATAACTA TTACTCACCT CTTTCTGAGT TACGTACGGT GCCCTCCACA
 98   I  L  K   S  I  D   N  E  W   R  K  T   Q  C  M   P  R  E   V  C


781 GTATAGATGT GGGGAAGGAG TTTGGAGTCG CGACAAACAC CTTCTTTAAA CCTCCATGTG
    CATATCTACA CCCCTTCCTC AAACCTCAGC GCTGTTTGTG GAAGAAATTT GGAGGTACAC
118   I  D  V   G  K  E   F  G  V   A  T  N   T  F  F   K  P  P   C  V


    accI
841 TGTCCGTCTA CAGATGTGGG GGTTGCTGCA ATAGTGAGGG GCTGCAGTGC ATGAACACCA
    ACAGGCAGAT GTCTACACCC CCAACGACGT TATCACTCCC CGACGTCACG TACTTGTGGT
138   S  V  Y   R  C  G   G  C  C   N  S  E   G  L  Q   C  M  N   T  S


901 GCACGAGCTA CCTCAGCAAG ACGTTATTTG AAATTACAGT GCCTCTCTCT CAAGGCCCCA
    CGTGCTCGAT GGAGTCGTTC TGCAATAAAC TTTAATGTCA CGGAGAGAGA GTTCCGGGGT
158   T  S  Y   L  S  K   T  L  F   E  I  T   V  P  L   S  Q  G   P  K


961 AACCAGTAAC AATCAGTTTT GCCAATCACA CTTCCTGCCG ATGCATGTCT AAACTGGATG
    TTGGTCATTG TTAGTCAAAA CGGTTAGTGT GAAGGACGGC TACGTACAGA TTTGACCTAC
178   P  V  T   I  S  F   A  N  H   T  S  C   R  C  M   S  K  L   D  V


1021 TTTACAGACA AGTTCATTCC ATTATTAGAC GTTCCCTGCC AGCAACACTA CCACAGTGTC
     AAATGTCTGT TCAAGTAAGG TAATAATCTG CAAGGGACGG TCGTTGTGAT GGTGTCACAG
 198   Y  R  Q   V  H  S   I  I  R   R  S  L   P  A  T   L  P  Q   C  Q


           •
1081 AGGCAGCGAA CAAGACCTGC CCCACCAATT ACATGTGGAA TAATCACATC TGCAGATGCC
     TCCGTCGCTT GTTCTGGACG GGGTGGTTAA TGTACACCTT ATTAGTGTAG ACGTCTACGG
 218   A  A  N   K  T  C   P  T  N   Y  M  W   N  N  H   I  C  R   C  L
```

```
1141 TGGCTCAGGA AGATTTTATG TTTTCCTCGG ATGCTGGAGA TGACTCAACA GATGGATTCC
     ACCGAGTCCT TCTAAAATAC AAAAGGAGCC TACGACCTCT ACTGAGTTGT CTACCTAAGG
 238   A  Q  E    D  F  M    F  S  S    D  A  G    D  D  S  T    D  G  F  H

1201 ATGACATCTG TGGACCAAAC AAGGAGCTGG ATGAAGAGAC CTGTCAGTGT GTCTGCAGAG
     TACTGTAGAC ACCTGGTTTG TTCCTCGACC TACTTCTCTG GACAGTCACA CAGACGTCTC
 258   D  I  C    G  P  N    K  E  L    D  E  E    T  C  Q  C    V  C  R  A

1261 CGGGGCTTCG GCCTGCCAGC TGTGGACCCC ACAAAGAACT AGACAGAAAC TCATGCCAGT
     GCCCCGAAGC CGGACGGTCG ACACCTGGGG TGTTTCTTGA TCTGTCTTTG AGTACGGTCA
 278   G  L  R    P  A  S    C  G  P    H  K  E  L    D  R  N    S  C  Q  C

1321 GTGTCTGTAA AAACAAACTC TTCCCCAGCC AATGTGGGGC CAACCGAGAA TTTGATGAAA
     CACAGACATT TTTGTTTGAG AAGGGGTCGG TTACACCCCG GTTGGCTCTT AAACTACTTT
 298   V  C  K    N  K  L    F  P  S    Q  C  G    A  N  R  E    F  D  E  N

1381 ACACATGCCA GTGTGTATGT AAAAGAACCT GCCCCAGAAA TCAACCCCTA AATCCTGGAA
     TGTGTACGGT CACACATACA TTTTCTTGGA CGGGGTCTTT AGTTGGGGAT TTAGGACCTT
 318   T  C  Q    C  V  C    K  R  T    C  P  R  N    Q  P  L    N  P  G  K

1441 AATGTGCCTG TGAATGTACA GAAAGTCCAC AGAAATGCTT GTTAAAAGGA AAGAAGTTCC
     TTACACGGAC ACTTACATGT CTTTCAGGTG TCTTTACGAA CAATTTTCCT TTCTTCAAGG
 338   C  A  C    E  C  T    E  S  P    Q  K  C  L    L  K  G    K  K  F  H

                                    eaeI
1501 ACCACCAAAC ATGCAGCTGT TACAGACGGC CATGTACGAA CCGCCAGAAG CTTGTGAGC
     TGGTGGTTTG TACGTCGACA ATGTCTGCCG GTACATGCTT GGCGGTCTTC CGAACACTCG
 358   H  Q  T    C  S  C    Y  R  R    P  C  T  N    R  Q  K    A  C  E  P

1561 CAGGATTTTC ATATAGTGAA GAAGTGTGTC GTTGTGTCCC TTCATATTGG AAAAGACCAC
     GTCCTAAAAG TATATCACTT CTTCACACAG CAACACAGGG AAGTATAACC TTTTCTGGTG
 378   G  F  S    Y  S  E    E  V  C    R  C  V    P  S  Y  W    K  R  P  Q

                                    claI
1621 AAATGAGCTA AGATTGTACT GTTTTCCAGT TCATCGATTT TCTATTATGG AAAACTGTGT
     TTTACTCGAT TCTAACATGA CAAAAGGTCA AGTAGCTAAA AGATAATACC TTTTGACACA
 398   M  S  O

1681 TGCCACAGTA GAACTGTCTG TGAACAGAGA GACCCTTGTG GGTCCATGCT AACAAAGACA
     ACGGTGTCAT CTTGACAGAC ACTTGTCTCT CTGGGAACAC CCAGGTACGA TTGTTTCTGT
```

FIGURE 1D

```
1741 AAAGTCTGTC TTTCCTGAAC CATGTGGATA ACTTTACAGA AATGGACTGG AGCTCATCTG
     TTTCAGACAG AAAGGACTTG GTACACCTAT TGAAATGTCT TTACCTGACC TCGAGTAGAC

1801 CAAAAGGCCT CTTGTAAAGA CTGGTTTTCT GCCAATGACC AAACAGCCAA GATTTTCCTC
     GTTTTCCGGA GAACATTTCT GACCAAAAGA CGGTTACTGG TTTGTCGGTT CTAAAAGGAG

1861 TTGTGATTTC TTTAAAAGAA TGACTATATA ATTTATTTCC ACTAAAAATA TTGTTTCTGC
     AACACTAAAG AAATTTTCTT ACTGATATAT TAAATAAAGG TGATTTTTAT AACAAAGACG

1921 ATTCATTTTT ATAGCAACAA CAATTGGTAA AACTCACTGT GATCAATATT TTTATATCAT
     TAAGTAAAAA TATCGTTGTT GTTAACCATT TTGAGTGACA CTAGTTATAA AAATATAGTA

1981 GCAAAATATG TTTAAAATAA AATGAAAATT GTATTAAAAA AAAAAAAAAA A
     CGTTTTATAC AAATTTTATT TTACTTTTAA CATAATTTTT TTTTTTTTT T
```
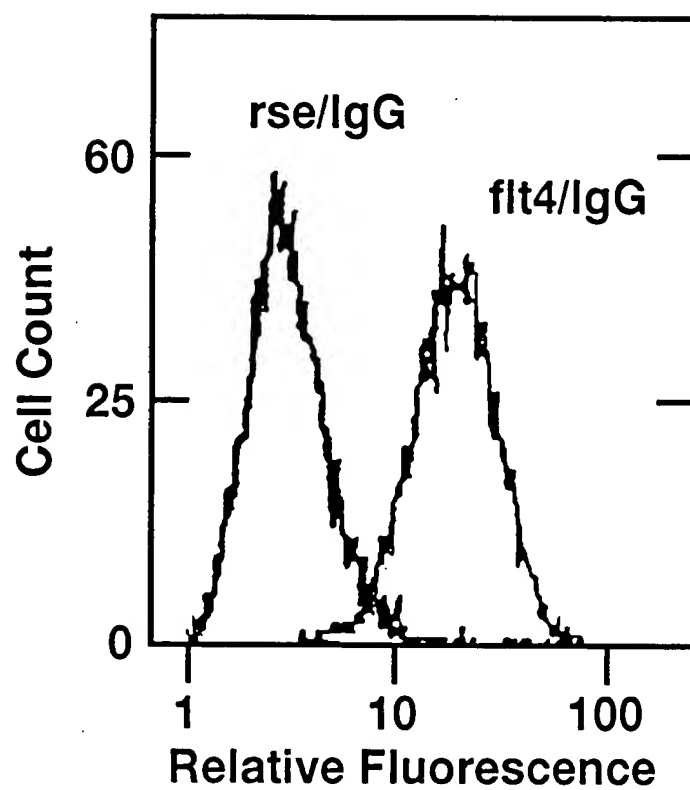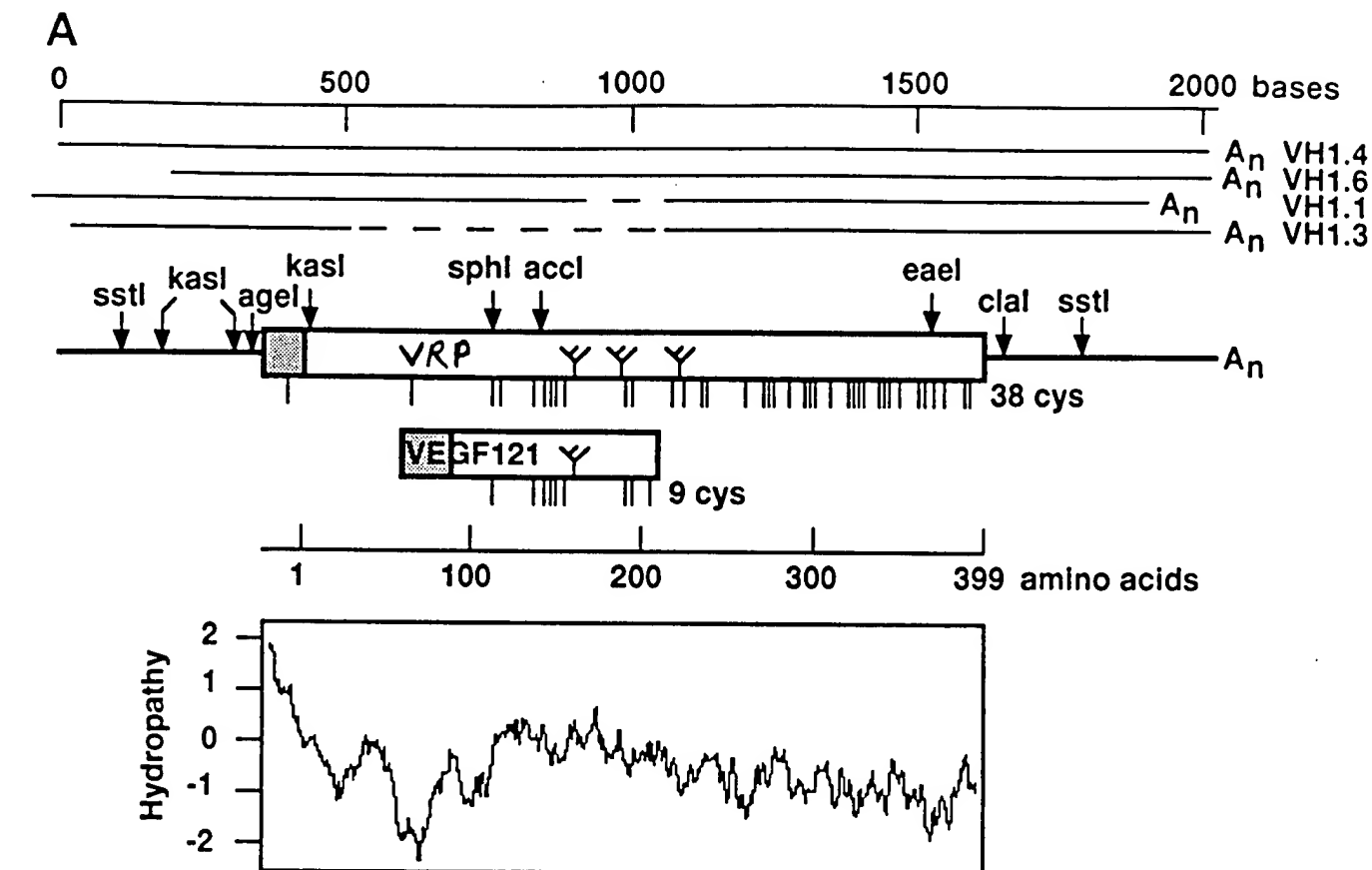
Figure 2

A

0   500   1000   1500   2000 bases

————————————————————————— An VH1.4
————————————————————————— An VH1.6
————————————————— An VH1.1
————————————————— An VH1.3

sstl kasl agel kasl sphl accl eael clal sstl

VRP

38 cys

VEGF121

9 cys

1   100   200   300   399 amino acids

Hydropathy
2
1
0
-1
-2

B

| VRP | -20 | M H L L G F F S V A C S L L A A A L L P G P R E A P A A A A A F E S G L D L S D A E P D A G E A T A |

VRP	31	Y A S K D L E E Q L R S V S S V D E L M T V L Y P E Y W K M Y K C Q L R K G G W Q H N R E Q A N L N
VEGF121	-26	- M N F L L S W V H W S L A L L L Y L H H A
PlGF131	-18	- - - - - - - - - - - - - - - - - M P V M R L F P C F L Q L L A G L A L P A

VRP	81	S R T E E T I K F A A A H Y N T E I L K S I D N E W R K T Q C M P R E V C I D V G K E F G V A T N T
VEGF121	-5	K W S Q A A P M A E G G G Q N H H E V V K F M D V Y Q R S Y C H P I E T L V D I F Q E Y P D E I E Y
PlGF131	4	V P P Q Q W A L S A G N G S S E V E V V P F Q E V W G R S Y C R A L E R L V D V S E Y P S E V E H

VRP	131	F F K P P C V S V Y R C G G C C N S E G L Q C M N T S T S Y L S K T L F E I T V P L S Q G P K P V T
VEGF121	46	I F K P S C V P L M R C G G C C N D E G L E C V P T E E S N I T M Q I M R I K P - - H Q G Q H I G E
PlGF131	54	M F S P S C V S L L R C T G C C G D E N L H C V P V E T A N V T M Q L L K I R S - - G D R P S Y V E

VRP	181	I S F A N H T S C R C M S K L D V Y R Q V H S I I R R S L P A T L P Q C Q A A N K T C P T N Y M W N
VEGF121	94	M S F L Q H N K C E C R P K K D R A R Q E K C D K P R R
PlGF131	102	L T F S Q H V R C E C R P L R E K M K P E R C G D A V P R R

| VRP | 231 | N H I C R C L A Q E D F M F S S D A G D D S T D G F H D I C G P N K E L D E E T C Q C V C R A G L R |

| VRP | 281 | P A S C G P H K E L D R N S C Q C V C K N K L F P S Q C G A N R E F D E N T C Q C V C K R T C P R N |

| VRP | 331 | Q P L N P G K C A C E C T E S P Q K C L L K G K K F H H Q T C S C Y R R P C T N R Q K A C E P G F S |

| VRP | 381 | Y S E E V C R C V P S Y W K R P Q M S |

Figure 3

ss.humvh1.nc, 1 to 2122

ss.HSC1WF111.nc, 844 to 1142

ss.H07991.nc, 844 to 1347

ss.H05177.nc, 845 to 1405

ss.T81690.nc, 1184 to 1686

ss.T84377.nc, 1185 to 1571

ss.T81481.nc, 1632 to 2108

ss.H05134.nc, 1658 to 2118

ss.R77495.nc, 1684 to 2074

ss.H07899.nc, 1698 to 2120

ss.HSC1WF112.nc, 1784 to 2108

ss.T89295.nc, 1901 to 2079

2,122 1,900 1,800 1,631 1,500 1,348 1,200 900 600 300

coding
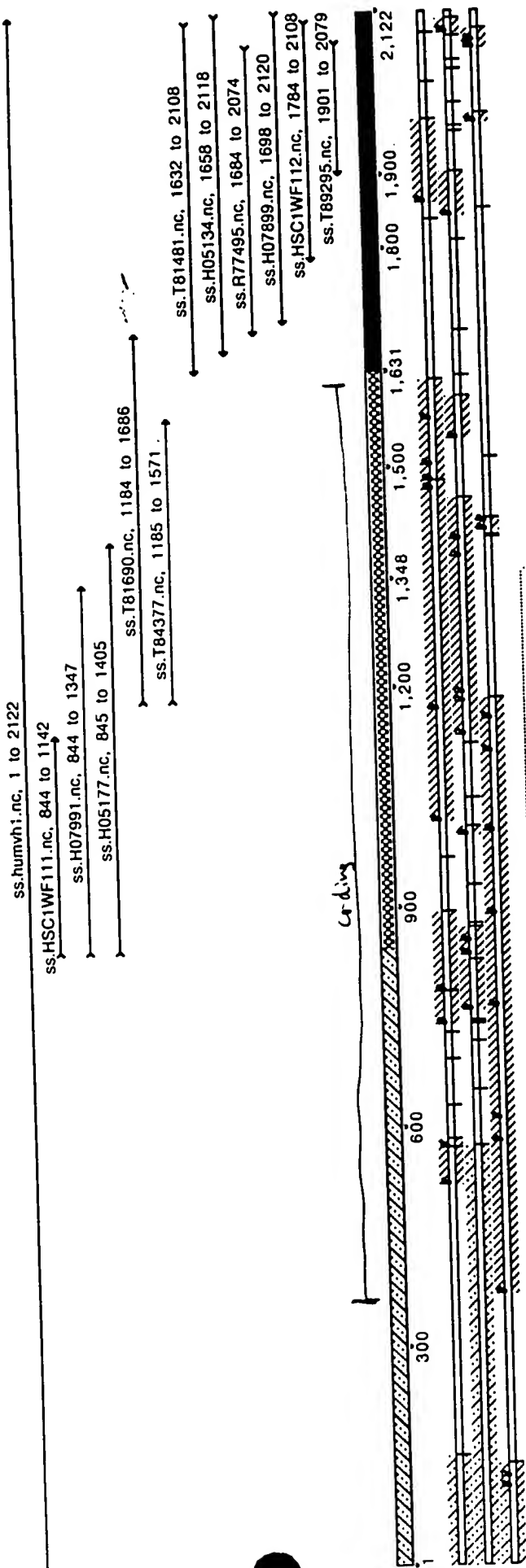
Diagram Key

- Hole in contig
- Single fragment
- Multiple fragments same direction
- Both strands
- Both strands plus
- Start codon frame 1
- Stop codon frame 2

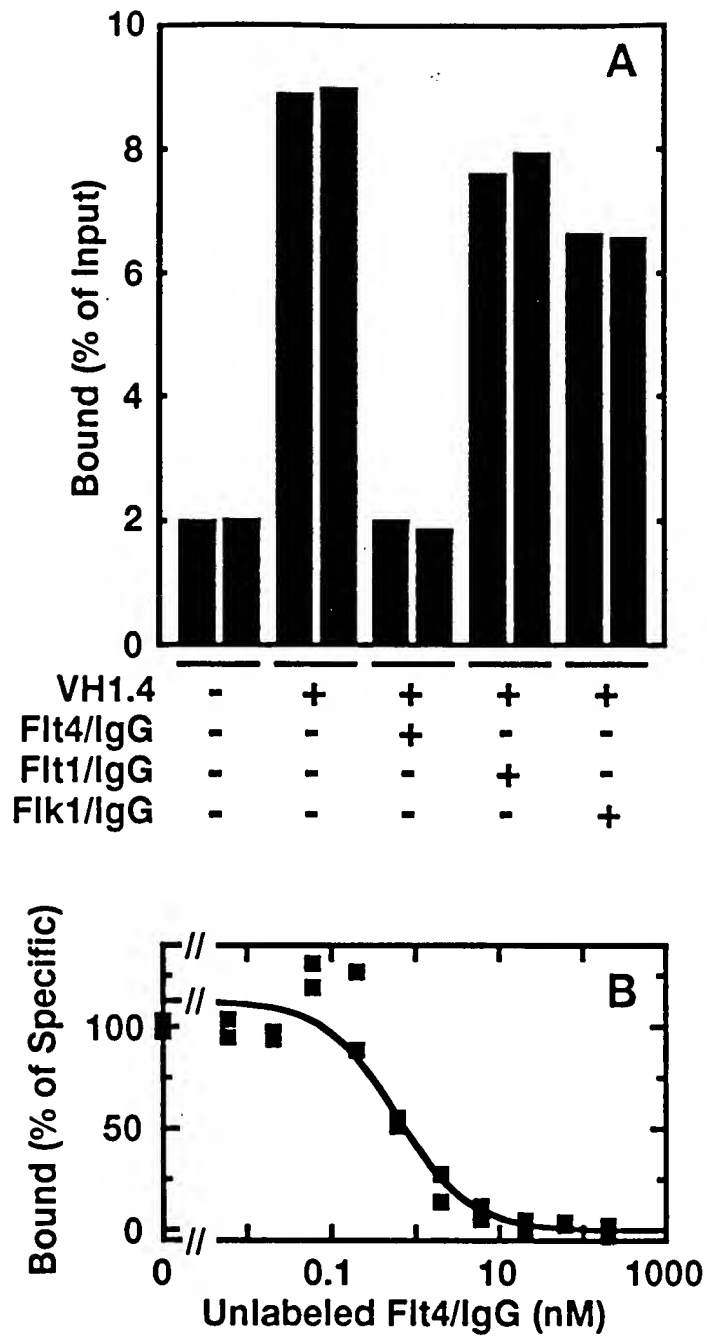Bumps on fragments show motifs, hollow rectangles show features

Figure 5

FIG. 6